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Listing first 45 summaries
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BQ636767
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4101.602 Million cell updates/sec
BQ636767 he01b10.y
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856250 K-E	BM8562	10	5	82	2
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068336 AV068	AV06833	2	ა	ω	5
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64715 AV06	AV06471	96	0	90.4	8
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512376 vj18c	AA51237	8	۲.	9	8
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70840 AV070	AV07084	87	ω	14.	4
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12489 RZPD Mus	BX51248	20	7.	20.	7
8 vn56e05.	AA59131	61	7.		6
23442 vp40a09.	AA82344	52	7.	20.	5
92439 vtš9c08.r	AA69243	30	7.	20.	4
136647 uq47b05	BE1366	18	7.	20.	ω
89871 vt6	AA68987	13	7.	20.	2
82819 vt57b03.	AA98281	85	7	20.	Ξ
009059 EST20351	AI009059	33	0	27.	0
223030 lJEJ18G	CB2230	25		30.	9
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732343 nf80b04.	AI73234	20	1	165.2	7
438 nf80b04.s	AA534438	21	ω	67.	σ
E543478 60	BE5434	15	0	ထ	u

ALIGNMENTS

JOURNAL COMMENT RESULT 1 BQ636767 LOCUS SOURCE ORGANISM REFERENCE DEFINITION KEYWORDS VERSION ACCESSION TITLE AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A., Touchman, J.W., Bouffard,G., Smith,D. and Peterson,K. Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal cDNA and alternative splicing of other retina-preferred gene transcripts Mol. Vis. 8 (4), 20021 In press BQ636767

334 bp mRNA linear EST 15-JUL-2002 he01b10.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he Homo sapiens cDNA clone he01b10 5', mRNA sequence.
BQ636767
BQ636767.1 GI:21761226 Tel: 301 402 3452 Fax: 301 496 0078 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 334) National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, Section on Molecular Structure and Function Homo sapiens Homo sapiens (human) graeme@helix.nih.gov 01 row: b column column: 10 the NEIBank and alternative

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JOURNAL COMMENT
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Email: yongsung@mail.kribb.re.kr
Plate: 51 row: E column: 10
High quality sequence stop: 355.
Location/Qualifiers
                                                                                                                                                     Genome Research Center
                                                                                                                                                                                                                               Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 355)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R
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                                                                                                                               Korea Research Institute of Bioscience & Biotechnology
                                                                                                                                                                           Contact: Kim YS
                                                                                                                                                                                           Unpublished
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l: +82-42-860-4470
x: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Retina"
/dev_stage="Adult"
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/mol_type="mRNA"
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Location/Qualifiers
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                               3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                            Contact: Scott J. Cain
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/db_xref="taxon:9606"
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Pred. No. 5.2e-45;
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                                                                                                                                                                                                                                                    Unpublished
Contact: John Quackenbush
The Institute for Genomic Research
The Institute for Jr., Rockville,
                                                                                                                                                                                                                                 9712 Medical Center Dr., Tel: 301 838 3528 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW960685 553 bp mRI
EST372756 MAGE resequences, MAGF Homo
AW960685
                                                                                                                                                                                                                                                                                                                Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray
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                                                                                                                                                                                                                                                                                                                                               Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                        Hegde, P., Qi, R., Abernathy, K.,
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%;
Conservative (
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                                                                  /mol_type="nRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGF"
/note="Vector: pBluescriptSKm"
153 c 137 g 107 t
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/note="See 'Creation of Genome-wide Protein Expression
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Score 180; DB 10;
Pred. No. 6.1e-45;
Mismatches 0;
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Pred. No. 6e-45;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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601070792F1 NIH_MGC_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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BE543478.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM8445 row: h column: High quality sequence stop: 385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                  GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGT
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                              CTCTGCTTGGCCCGGATAAAAACCAAACAGGACATCCAGATCATGAAAGATGGCAAATGC
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300 c 247 g 88 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NIH_MGC_12"
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Pred. No. 7.8e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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O.
                                                                        GCTCTGCTTGGCCCGGATAAAAACCAAACAGGACATCCAGATCATGAAAGATGGCAAATG
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/note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. "
                                                                                                                                                                                                                                                                                                                                                                                                                              normalization.
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/lab_host="DH10B"
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/clone="IMAGE:926191"
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/mol_type="mRNA"
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Best Local
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58
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nf80b04.x5
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Insert Length: 417 Std
Seq primer: -400P from Gi
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Anatomy Project (CGAP), Tumor Gene Index
This read has been verified (found to hit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: National Cancer Institute, Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Grey Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AI732343
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                                                                                                   GGAAAGCTCCCTTTTTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCGACCTGT 119
CTCTGCTTGGCCCGGATAAAAAACCAAACAGGACATCCAGATCATGAAAGATGGCAAAT 1
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/rote="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. "
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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/sex="pooled"
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NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926191
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Pred. No. 1.7e-40;
""" matches 8;
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RESULT 1
AR166137
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AR166137 180 bp Sequence 1 from patent US 6280968. AR166137

DNA

linear

PAT 17-OCT-2001

AR166137.1

GI:16241312

REFERENCE AUTHORS TITLE

1 (bases 1 to 180)

Kato, S., Yamaguchi, T., Sekine, S. and Kamata, Human PEC-60-like protein and DNA encoding t Patent: US 6280968-A 1 28-AUG-2001;

Location/Qualifiers

the

same

FEATURES

SOURCE ORGANISM

Unknown. Unknown. Unclassified. score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result a C a 00 Score Query Match 67.1 65.2 65.2 65.2 45.1 45 163396 176584 183099 188540 192093 230493 242175 Length 482 5635 168 182 182 182 182 186 DВ 9 5 5 5 6 7 6 9 0 9 ი ი 9 SYNPSTIAA A24907 E03479 SYNECOPST BC025790 AR270687 AX332609 AX333248 AX411203 BD160949 A11350 A11352 A24905 AC011108 AC121205 AL837521 MMMPGC60 AL161445 AC027812 AC034144 S46866 SSPEC60 AR166137 E13090 AF048700 AR028526 AR075817 BD007521 MMPIMP12 E01725 AC096463 I08731 AR166138 E13091 HSPSTI E08411 E03120 AR059723 AX014851 SYNPSTIB **ASVPSKAN8** ALIGNMENTS Y00705 Homo sapien X06342 Mouse mRNA E01725 Synthetic D E02456 DNA encodin M31103 Synthetic h AL161445 Human DNA AC027812 Homo sapi AC034144 Homo sapi AC011108 Homo sapi AC011108 Tantus no AL837521 Mouse DNA AC096463 Rattus no 108731 Sequence 19 A11350 Artificial A11352 Artificial A14905 PSTI master M21832 Synthetic h A24907 DSNA encodi X84307 Artificial AF048700 Homo sapi AR028526 Sequence AR075817 Sequence BD007521 Tumor-ass \$46866 PEC-60=gast X67109 S.scrofa PE Y11505 M.musculus AR166138 Sequence E13091 Human cDNA AX014851 Sequence AR166137 Sequence E13090 Human an cD M11949 Human BC025790 Homo sapi AR270687 Sequence E01574 cDNA sequen M22196 Synthetic E AR059723 Sequence E08411 DNA sequenc E01819 DNA sequenc E03120 DNA sequenc Description

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PD 13-M2
PF 27-OC
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PC (C
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SAGAMI CHEM RES CENTER
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Kato, M., Yamaguchi, T., Sekine, S. and Kamata, M.
HUMAN PEC-60LIKE PROTEIN AND DNA CAPABLE OF CODING THE SAME Patent: JP 1997124698 A 1 13-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human an cDNA encoding E13090
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                                              GGAAAGCTCCCTTTCTCAAGAATGCCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGT
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JP 1997124698-A/1
13-MAY-1997
27-OCT-1995 JP 1995280272
KRATO MASASHI, YAMAGUCHI TOMOKO, SEKINE SHINGO,
                                                                                                                                                                                                                                                                53
                                                                                                                                             Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
49 c 40 g 3
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/organism="unknown"
49 c 40 g
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/tissue_type='stomach cancer'
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                                                                                                                                      Score 180; DB 6;
Pred. No. 2.6e-47;
; Mismatches 0;
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-60-like protein.
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RESULT 4
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Submitted (17-FEB-1998)
Yue-Yang Road, Shanghai
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Mammalia; Eutheria; Primates;
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/codon_start=1
/product="gastrointestinal peptide"
/protein_id="AACO5124.1"
/protein_id="AACO5440"
/db_xref="G1:2935440"
/translation="MAVRQWVIALALAALLVVDREVPVAAGKLPFSRMPICEHMVESP
TCSQMSNLVCGTDGLTYTNECQLCLARIKTKQDIQIMKDGKC"
97 c 98 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 2.6e-47;
; Mismatches 0;
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BD007521.1 GI:18635894

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Sequence 2 1
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Bandman,O., Goll,S.K. and Murry,L.E.
Tumor-associated Kazal inhibitor
Patent: US. 4958699-A 2 28-SEP-1999;
Location/Qualifiers
1. 388
                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
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Patent: US 5858
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Bandman,O., Goli,S.K. and Murry,L.E.
Tumor-associated kazal inhibitor-like
                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AR075817.1
                                                                                                                                                                                                                                                                                                                                                                                             Unclassified
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                                                                                                     CTCTGCTTGGCCCGGATAAAAACCAAACAGGACATCCAGATCATGAAAGATGGCAAATGC
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Location/Qualifiers
1. 388
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105 c 102 g
                                                                                                                                                                                                                                                                                                /organism="unknown"
105 c . 102 g
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                                  388
type
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Pred. No. 2.6e-47;
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                                               PAT 31-JAN-2002
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REFERENCE
AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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AR166138
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Query Match
Best Local Similarity
Matches 180; Conser
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PN JP 2001503629-A/1
PD JP 06-NOV-1997 JP 1998521770
PR 06-NOV-1996 US 08/744670
PR 06-NOV-1996 US 08/744670
PR C12N15/09, A61N38/55,A61N39/395,A61P1/00,A61P35/00,C07K14/81,
PC C12N15/09,A61N38/55,A61N39/395,A61P1/00,A61P35/00,C07K14/81,
PC C12N17/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/574, PC C12N15/00,C12N5/00,
PC A61K37/64
CC A61K37/64
FT Source /organism='Unidentified'.
FT Source /organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                         111 GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGT
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Sequence 2 :
AR166138
AR166138.1
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Bandman,O., Goli,S.K. and Murry,L.E.
Tumor-associated KAZAL type inhibitor
Patent: JP 2001503629-A 1 21-MAR-2001;
INCYTE PHARMACEUTICALS INC
                                                                                                                  Kato.S., Yamaguchi,T., Sekine,S. and Kamata,
Human PBC-60-like protein and DNA encoding t
Patent: US 6289958-A 2 28-AUG-2001;
Location/Qualifiers
                                                                                                                                                                                                          Unknown.
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100.0%; ilarity 100.0%; Conservative 0;
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05-NOV-1997 JP 1998521770

06-NOV-1996 US 08/744670

OLGA BANDMAN, SURYA K GOLI, LYNN E MURRY

C12N15/09, A61K38/55, A61K39/395, A61F1/00, A61F35/00, C07K14/81,

C07K16/38,
                                                                        /organism="unknown"
110 c 105 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
105 c 102 g 7
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Score 180; DB 6;
Pred. No. 2.6e-47;
; Mismatches 0;
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Pred. No. 2.6e-47;
Mismatches 0;
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1 GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGT 60

PAT 07-SEP-2000

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RESULT 8
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PN JP 19
PN JR 13-MA
PF 27-OC
PF KATO
MITSUHISA
PC C07K1
PC C12P2
PC (C12P2
PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato, M., Yamaguchi, T., Sekine, S. and Kamata, M. HUMAN PEC-60LIKE PROTEIN AND DNA CAPABLE OF CODING PATENT: JP 197124698-A 2 13-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAGAMI CHEM RES CENTER
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(bases 7 to 398)
(bases 1 to 398)
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ilarity 100.0%;
Conservative (
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
110 c 105 g 7
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PEC-60-like protein
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Pred. No. 2.6e-47;
; Mismatches 0;
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AUTHORS
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                                                                                                                                                                                                                                "ecsis,M., Cintra,A., Solfrini,V., Ernfors,P.,
Morrasutti,D.G., Ostenson,C.G., Efendic,S., Ag
et,al.
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Sequence 41 from Patent W09953040.
AX014851
                                                                                         GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 115614] from the original journal article. This sequence comes from Fig. 1.
                                                                                                                                                               Molecular cloning of PEC-60 and expression of its in the gastrointestinal tract and immune system J. Biol. Chem. 267 (28), 19829-19832 (1992) 93015834
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
1 (bases 1 to 364)
Metsis,M., Cintra,A.,
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PEC-60=gastrointestinal
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                                                                                                                                                                                                                                                                                                                                                Sus scrofa
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
111 c 107 g 7
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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05-AUG-1999 364 nt].

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mRNA and peptide

Euteleostomi;
Sus.

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                                                                                                                                                                                                                                                                                                                                                                        pec-60 gene.
Sus scrofa (pig)
                                                                                                                                                                                                                                                                              Submitted (22-JUN-1992) M. of Molecular Neurobiology,
                                                                                                                                                                                                                                                                                                                                                                                                                  S.scrofa PEC-60 mRNA
X67109
                                                                                                                                                                                                                                                                       Stockholm,
                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
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1 (bases 1 to 364)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mavrlwvvalalaalfivdrevpvsaekqvfsrmpicehmtesp
DCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGEC"
93 c 108 g 72 t
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93 c 108 g 72
                                                          /note='
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                                                                                                                             /product="peptide PEC-60"
/protein_id="CAA47482.1"
/db_xref="GI:2034"
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                                                                                                                                                                                                                       /organism="Sus scrofa"
/mol_type="mRNA"
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/db_xref="GI:5705936"
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                                                                                                                                                               /evidence=experimental
                                                                                                                                                                         /codon_start=1
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81.7%;
  70.78;
                                                                     peptide PEC-60"
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                                                                                                                                                                                                                                                                                 Metsis, Dept. of Medical Chemistry, Lab
Karolinska Institute, Box 604 00, 10401
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143; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-FEB-1997) R. Krause, Ropers, Ihnestr. 73, 14195 Berlin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krause, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krause,R., Hemberger,M., Messerschmid,M., Kothary,R. and Fundele,R. Molecular cDNA cloning and expression of murine Mpgc60, a gene predominantly expressed in the intestinal tract
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predominantly expressed
                                                   GGGAGCCTTGTTTTCCCCAGAATGCCCTTCTGTGAGCACATGGCTGAGCTTCCAAACTGT
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                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                    /product="M9960 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sub_strain="Hannover (random bred)"
/db_xref="taxon:10090"
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/dev_stage="adult"
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79.48;
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                                                                                                                                                                         Score 120.8; DB 10;
Pred. No. 4.4e-28;
0; Mismatches 37;
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); Mismatches
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ches 33;
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AL161445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/HGP/Chr9
This sequence is the entire insert of clone RP11-326F20 The true right end of clone RP11-34AB24 is at 100362 in this sequence. The true right end of clone RP11-54K16 is at 54767 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-326F20 is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Nov 10, 2000 this sequence version replaced gi:11071610.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL161445

163396 bp DNA linear PRI 04-DEC-2001

Human DNA sequence from clone RPII-326F20 on chromosome 9 Contains

the GGTA1 gene for glycoprotein alpha-galactosyl transferase 1, the

SPINK4 gene for Kazal type 4 serine protease inhibitor, the 3' end

of the BAG1 gene for BCL2-associated athanogene and a CpG island,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; athanogene; BAG1; BCL2;
GGTA1; glycoprotein; Kazal; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the library RPCI-11.2 constructed by the group of Pieter de Jong For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ramsay, H
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pBACe3.6.
                                                                 /note="MER44A repeat: matches 225.
440. .555
                                                                                                                                                                                           /note="AluY repeat: matches 77. .309 of consensus" 239. .314
                                                                                                                                /note="L1M4 repeat: matches 2591.
331. .438
                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                        /clone="RP11-326F20"
                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
                             'note="AluSq/x repeat: matches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .163396
                                                                                                                             .438
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serine protease inhibitor; SPINK4.
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                                                                                            .331 of consensus"
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8784..9
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8462..8
                                                     complement(join(14283.
                                                                                      /note="MIR repeat: matches 112. .257 of consensus"
complement(14283. .70891)
                                                                                                                                                                                                                                                                                                        /note="9 copies 10 mer gtgtgtgtt 72% conserved"
complement(12461, .12790)
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="FLAM_C
12121 12219
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MIR repeat: matches 132. .252 of consensus" 11874. .12110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSp repeat: 9086. .9106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1. .304 of consensus" 8770. .8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 81.
7523. .7596
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3046. .3192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .301 of consensus"
1982. .2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluJo/FRAM repeat: matches 158. .298 of consensus' 795. .1193
                                                                                                                             14033.
                                                                                                                                                                /note="FLAM_A repeat: matches 1.
13290. .13517
                                                                                                                                                                                                                                                                   complement(12571
                                                                                                                                                                                                                                                                                                                                               /note="52 copies 2 mer tg 71% conserved"
12254. .12343
                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 35.
12243. .12346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10464.
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1194 . .1491
                                                                                                                                                                                                   13171.
                                                                                                                                                                                                                                                    note="match: GSS: Em:AQ177335"
                                                                                                                                                                                                                                                                                       note="match: GSS: Em:AQ210501"
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/note="L1MB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L1P1 repeat: matches 5753. .5825 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluSq repeat:
4863. .5008
/product="bA326F20.1 (glycoprotein, alpha-galactosyl
                                                                                                                                          'note="MER21B repeat: matches 4.
                                                                                                                                                                                                                 note="MER21B repeat: matches 232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="MIR repeat: matches 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER41B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="MER41B repeat: matches 150. .635 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluJb repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluSp repeat: matches 1, .296 of consensus"
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                                  .24252,38835.
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                                                                                                                                                                                                                                                                         .12678
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                                    .39070,70404. .70891))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matches 1. .302 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 1. .304 of consensus"
                                                     .17232,17420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .130 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .147 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  .142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .138 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2742 of
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                                                                                                                                             .232 of consensus"
                                                                                                                                                                                .122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4701 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of consensus"
                                                                                                                                                                                                                   .794 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6184 of consensus"
                                                     .17524,19637. .19759,
                                                                                                                                                                              of consensus"
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                                                                                          150244 CTCCCTTCTTCCACAGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAG
                                                                                                                                                                                                            Local
                     Similarity
                                                                                                               CTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAG 66
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="glycoprotein, alpha-galactosyl transferase 1 match: cDNAs: Em:J03880 Em:D00314 Em:E02227 Em:M13569 Em:X14085 Em:A23697 Em:X14558 Em:M22921 Em:G10473 Em:E02228 Em:X1323 Em:D0314 Em:S5415 Em:U19890 Em:X12510 Em:M13701 Em:G19889 Em:AF038660 Em:M13701 Em:G19889 Em:AF038660 Em:U10474 Em:AB024434 Em:AB019541 Em:U10472 Em:AF142670 Em:U10474 Em:BF124086 Em:AM467118 Em:AR149377 Em:AA476930 Em:AB1192425 Em:AL572046 Em:AL149377 Em:AA476930 Em:AAA889902 Em:AL502465 Em:AW362033 Em:AL149203 Em:AL149275 Em:AA889902 Em:AL5028425 Em:AW362033 Em:AL149203 Em:AL1655973"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17946. .18109
/note="L2 repeat: matches 2241. .2411 of consensus"
19126. .19243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/product="ba326F20.1 (g1ycoprotein, alpha-galactosyl
transferase 1)"
/protein_id="CAD13306.1"
/db_xref="G1:17384434"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mrlrepilsgsaampgaslqracrilvavcalhigvtlvyylag
RDLSRLPQLVGVSTPLQGGSNSAAAIGQSSGELRTGGARPPPPLGASSQPRPGGDSSP
VVDSGPGPASNLTSVPVPHTTALSLPACPEESPLLVGPMLIEFNMPVDLELVAKQNPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="19 copies 2 mer aa 92% conserved"
complement(15755. .17099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFSLPYVQYFGGVSALSKQQFLTINGFPNNYWGWGGEDDDIFNRLVFRGMSISRPNAV
VGRCRMIRHSRDKKNEPNPQRFDRIAHTKETMLSDGLNSLTYQVLDVQRYPLYTQITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTIFNRAKLLNVGFQEALKDYDYTCFVFSDVDLIPMNDHNAYRCFSQPRHISVAMDKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKMGGRYAPRDCVSPHKVAIIIPFRNRQEHLKYWLYYLHPVLQRQQLDYGIYVINQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(17100.
24065. .24252,38835. .:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="GGTA1"
complement(14305. .14310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
complement(14283)
/gene="GGTA1"
                                                                                                                                                                                                                                                                                               /note="AluJb repeat: matches 1.
24409. .24625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1MC5 repeat: matches 7805. .7927 of consensus"
19877. .20157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: proteins: Tr:060512"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: STS: Em:G05861"
                                                                                                                                                                                                                                                                          /note="L1ME
                                                                                                                                                                                                                                                                                                                                                               /note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluSc repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="match: STS: Em:G59840"
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91.9%;
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                                                                                                                                                                                                                                                                       repeat: matches 5615. .5826 of consensus"
                                                                                                                                                                                                     Score 117.4; DB 9
Pred. No. 5.3e-27;
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0. .17232,17420. .17524,19637. .19759,
.39070,70404. .70815))
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                                                                                                                                                                                                                                                                                                                     .305 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                  .297 of consensus"
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                                                                                                                                                                                                                                                                                                                    Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vioung, G., Zainoun, J., Zimmer, A., and Zody, M.
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Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karratas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Voung, G., Zainoun, J., Zimmer, A. and Zody, M.
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Homo sapiens chromosome 9 clone
SEQUENCE, 29 unordered pieces.
AC027812
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 2, 2000 this sequence version replaced gi:7382654. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 176584)
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                                                                                                                                                                                                                                                                                        Direct Submission
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 162821 bases at least Q40
Consensus quality: 162946 bases at least Q30
Consensus quality: 172552 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 173784; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 182699; sum-of-contigs
Quality coverage: 6.27 in Q20 bases; agarose-fp
Quality coverage: 6.20 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-primer ET; 100% of reads chemistry: Dye-terminator Big Dye; 0% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 179431 bases at least 040 Consensus quality: 180878 bases at least 030 Consensus quality: 181543 bases at least 020 Consensus quality: 181543 bases at least 020 Consensus quality: 181543 bases at least 020
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Submitted (04-APR-2000) Genome Sequencing Center, Washington
Submitted (04-APR-2000) Genome Sequencing Center, Washington
Of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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/mol_type="genomic DNA"
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13-DEC-2002 (first entry) ABVBBBB5;

Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine; gene; Human colon cancer related cDNA SEQ ID NO 206

ARESIS 20-NOV-2000; 06-FEB-2001; 28-MAR-2001; 10-JUL-2001; WPI; 2002-608400/65. Stolk JA, WO200258334-A2 Homo saptens 01-AUG-2002 (CORI-) CORIXA CORP. 19-NOV-2001; 2001WO-US43704. Xu J, Chenault RA, ; 20000%-252222P. ; 2001US-267011P. ; 2001US-29670P. ; 2001US-304837P. Meagher MJ,

Secrist H, King GE;

New isolated tumor diagnosis, preventi

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and/or

polynucleotide and polypeptide, useful d/or treatment of cancer, in particular

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   New isolated tumor colon polynucleotide
                           WPI; 2002-608400/65.
                                                   Stolk
                                                                                             20-NOV-2000; 2000US-252222P.
06-FEB-2001; 2001US-267011P.
28-MAR-2001; 2001US-279670P.
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                                                                                                                                                                                                                                                                                    cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 66 A; 81 C;
                                                                                                                                                        2001WO~US43704
                                                                                                                                                                                                                                                                                                         (first
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                                                                                                                                                                                                                                                            cancer; cytostatic;
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                                                 Chenault
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                                                                                                                                                                                                                                                                                   related
                                                                                                                                                                                                                                                                                                                                                       cDNA;
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                                                                                                                                                                                                                                                                                                         entry)
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                                                 RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 G; 83 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 180; DB 24;
Pred. No. 1.1e-51;
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                                                 Meagher
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                                                                                                                                                                                                                                                           tumour; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                   ID NO
   and
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polypeptide,
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  useful for
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RESULT 3
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Best Local (
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                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                            Human; tumbur-associated Kazal inhibitor; TAKI; inflammation; ulcerative calitis; Crohn's disease; inflammatory cytokine; elserine protease; glycoprotein hormone; trypsin; chymotrypsin;
                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                      14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                      AAV38073 standard;
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cancer -
                                Bandman O,
                                                                                 06-NOV-1996;
                                                                                                         05-NOV-1997;
                                                                                                                                14-MAY-1998
                                                                                                                                                        WO9820132-A1
                                                                                                                                                                                                                                          Homo
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                                                        (INCY-) INCYTE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGT
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                                 Goli SK,
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                                                                                                         97WO-US20204.
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Pred. No.
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                                                                                                                                                                                                                                                              pepsin;
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WPI; 1998-286948/25 P-PSDB; AAW62074.

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PR 31-J-F
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Best Local S
Matches 180
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09-FEB-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAKI). TAKI is expressed in response to inflammatory cytokines and functions in the inhibits of serine proteases or glycoprotein hormones present in diseased tissues. The TAKI can be used to inhibit the tissue destruction associated with the production of excess proteases such as trypsin, chymotrypsin, elastase, or pepsin. Products from the present invention can be used in the treatment of e.g. proliferative cell division in inflamed intestinal tixsues, ulcerative colitis, Crohn's disease or cancer. The products can also be used for detection and
                                                                                                                                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                        30-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                   08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; pancreas; can
cytostatic; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human pahcreatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         АВУ97573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV97573 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated tumour-associated Kazal inhibitor, TAKI - used develop products for the diagnosis and treatment of e.g. inflammation; ulcerative colitis, Crohm's disease or cancer
                                                                                    (CORI-)
                                                                                                                                                                            16-MAY-2001;
12-JUL-2001;
                                                                                                                                                                                                                       28-APR-2001;
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2001US-265682P.

2001US-267568P.

2001US-27851P.

2001US-28712P.

2001US-291631P.

2001US-3054844
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                                           Kalos MD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; gene therapy; vaccine;
ur; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer expressed cDNA SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                     -US02781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encodes human tumour-associated Kazal inhibitor
                                           Lodes
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                                         Rersing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc any of a group of over 4000 nucleotide sequences (ABV94628-ABV9145); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a) under cc contiguous residues of (a); (d) sequences that hybridize to (a) under cc contiguous residues of (a); (d) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides CC (ABP6859-ABP6863) encoded by (1) and oligonucleotide can be used to detect cancer in a patient had compositions comprising polypeptides, comply of the composition of the composition of the composition and antigen presenting cells expressing the polypeptide are useful in the creating pancreatic cancer and stimulating an immune response. The collypucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for composition of the tumour cells, in vaccines and for gehe therapy.

Note: The sequence data for this patcht did not form part of the printed content of the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and pancreatic for diagnosing, preventing and/or treating
                                     WO9715596-A1
                                                                                       mat_peptide
                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                              antigen;
                                                                                                                                                                                                                                                                                                nervous disorder;
                                                                                                                                                                                                                                                                                                                  Human; PEC-60-type protein; digestive disorder; immune disorder;
                                                                                                                                                                                                                                                                                                                                                       Human PEC-60-type protein encoding
                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT64673;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody;
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                          /*tag= a
/product=
43..120
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                                                                                                                                                                                   Location/Qualifiers 43..303
                                                                      /*tag=
                                                                                           121..300
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                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                              gastrointestinal tract hormone; gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA to
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Pred. No. 1.2e-51;
; Mismatches 0;
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cancer, particularly
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22-OCT-1996;

96WO-JP03061.

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a human PEC-60-type protein. The protein is a gastrointestinal tract hormone secreted by the gastric tissues. It is useful for treatment or diagnosis of digestive, immune or nervous disorders, or as an antigen to raise antibodies against them. Large amounts of the protein may be produced by using the corresponding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PEC-60-type protein - immune or nervous disorders
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P-PSDB; AAW15067.
    New nucleic
                                           P-PSDB; AAY76598,
                                                                    WPI; 1999-591920/51
                                                                                                                                                                                                 09-APR-1998;
                                                                                                                                                                                                                                               09-APR-1998;
                                                                                                                                                                                                                                                                                          21-OCT-1999.
                                                                                                                                                                                                                                                                                                                                     DE19817557-A1.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                               Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ77490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 10;
  acid
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                                                                                                                                                                                                                                                                                                                                                                                                                       treatment;
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                                                                                                                                                        GES GENOMFORSCHUNG MBH.
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sequences expressed
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                                             AAY76599.
                                                                                                                                                                                                                                                                                                                                                                                                                                              tag; EST; human; ovarian tumor; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA; 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 180; DB 18;
Pred. No. 1.2e-51;
Mismatches 0;
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ovarian,
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and
                                                                                                           Pilarsky
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other,
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags) from a particular tissue type before comparison of the expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAZT7450-Z77572 represent the human ovarian tumor cDNA library derived EST fragments described in the method of the invention and encode the protein fragments represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC98176 standard; cDNA; 433
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                                                                                                                                      08-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       neural disorder; immune system disorder; muscular disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                        nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosts; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary;
                                                                               12-MAR-1999;
                                                                                                                                                                                              21-SEP-2000
                                                                                                                                                                                                                                                      WO200055351-A1
                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                  reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC98176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory; muscular;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer antigen nucleotide sequence
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                                                                                                                                         2000WO-US05883
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                                                                                  99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  gynaecological; gastrointestinal;
; antibacterial; gene therapy; wound;
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Pred. No. 1.2e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
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Matches 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH34805 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary, nephrotropik, antiinfective and antibacterial activities, can be used in gene thekapy. The colon cancer antigen polynucleotides proteins and antibodies to the proteins are useful for the prevention treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins
                                                                                                          29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC97991 to AAC98063 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon cancer associated gene sequences, referred to antigens, useful for the treatment, prevention, and
                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                    28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCAGATGTCCAACCTGGTCTGCGGCACTGATGGGCTCA&ATATACGAATGAATGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; colon
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                                                                                                          99US-0157137.
99US-0163280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding cDNA SEQ ID NO:1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180;\
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 G;
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2e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. Additionally, N may be used to produce the colon cancer-associated Ps. By inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and N can be used in the prevention, diagnosis and treatment of colorectal carchomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the
                                                  02-OCT-2000; 2000US-237271P
                                                                                                    02-OCT-2001;
                                                                                                                                                         11-APR-2002
                                                                                                                                                                                                                                                                                                        genetic
                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer related nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2002
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N.B. Pages 666 to 682 and page 7053 of t missing at time of publication, meaning SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer-associated nucleic acid molecules (N) the proteins are collectively known as colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH32943 to AAH37195
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     (FARB ) BAYER CORP
                                                                                                                                                                                                      WO200229086-A2
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ60075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 433 BP; 133 A; 113 C; 110 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCTGCTTGGCCCGGATAAAAACCAAACAGGACATCCAGATÇATGAAAGATGGCAAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preventing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                    2001WO-US30732
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                           diagnostic; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA; 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                      cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and AAG73514 to AAG77788 represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4277 human colon cancer-associated polypeptides, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birse CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                   tissue profiling; forensic; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180; \I
Pred. No. 1.\
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Τ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ke-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences listing were sequences are present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:3770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGGTAGAGTCTCCAACCTGT
                                                                                                                                                                                                                                                                                                           gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc expressed in cancer tissues. ABB78993 to ABB79004 represent proteins cc encoded by the ABQ60787 to ABQ60787 nucleic acid sequences. (I) can be cused in antisense therapy. An antibody immunoreactive with a polypeptide cc encoded by (I) is useful for detecting cancer in a patient sample, and cc for detecting the presence of absence of a polynucleotide encoded by a cucleic acid which hybridises to (I) in a cell. A probe/primer derived cf from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived comparison to used for determining the presence of a nucleic acid which hybridises to (I) is useful for determining the presence of cc colon cancer in a cell or tissue type, for determining the presence or cc state of other type of cancer, in antisense therapy, to generate cc corresponding gene resides, and in tissue profiling, forensics, genetic cc analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Sin
Matches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid that is differentially expressed tissues useful for determining the presence of colon cancer or tissue type, and in antisense therapy .
                            02-OCT-2001; 2001WO-US30732
                                                                                  11-APR-2002
                                                                                                                                                                                                                                                genetic
                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ60577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ60577 standard; cDNA; 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgess C,
Thiaglingam
                                                                                                                                   WO200229086-A2
                                                                                                                                                                                                                                                                                                                             Human colon cancer related nucleotide sequence SEQ ID NO:4272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
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                                                                                                                                                                                                                                                                          colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 96.775; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGATGTCCAACCTGGTCTGCGGCACTGATGGGCTCACATATAC-GAATGAATGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTGCTTGGCCCGGATAAAAACCAACNAGGACATCCAAGATCATGAAAGATGGCAAATG
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n A, Lewis
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 A;
                                                                                                                                                                                                                                                diagnostic;
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96.7%;
                                                                                                                                                                                                                                                                          cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 C; 119 G;
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                                                                                                                                                                                                                                       tissue profiling; forensic; mapping;
; antisense therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 151.8; DB Pred. No. 6e-42; O; Mismatches,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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 09-OCT-1987;
                                                                                                                   Human pancreatic secretory trypsin inhibitor; pancreatic proteolytic zymogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid that is differentially expressed
tissues useful for determining the presence of colon cancel
or tissue type, and in antisense therapy
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                              05-MAY-1988
                                                                                     Homo sapiens
                                                                                                                                                                Sequence encoding novel human pancreatic secretory trypsin inhibitor (HPSTI).
                                                                                                                                                                                                              25-MAR-2003
17-SEP-1990
                                                                                                                                                                                                                                                            AAN80453;
                                                                                                                                                                                                                                                                                        AAN80453 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                   CTCTGCTTGGCCCGGATAAAAACCAAACAGGACATCCA 158
                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCANATGTCCAACCTGGTNTGCGGCACTGATNGGCTCACATATACAAATGAATGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGNTTGG-CCGNATAAAAACCAAACAGNACATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 1; 796pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type, and in antisense therapy
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(first entry)
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 87WO-US02585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JH,
                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.3%;
94.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 137.4; DB 24,
Pred. No. 4.3e-37;
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Result
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1: /cgn2_6/ptodata/1
2: //gn2_6/ptodata/1
3: /cgn2_6/ptodata/1
4: /cgn2_6/ptodata/1
5: //gn2_6/ptodata/1
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/cgn2_6/ptodata/1/ina/B_COMB.seq:*
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RESULT 2 US-08-744-670-2 US-08-744-670-2 ; Sequence 2, Application US/08744670 ; Patent No. 5858710 ; GENERAL INFORMATION: ; APPLICANT: Bandman, Olga APPLICANT: MUTTY, Lynn E. ; APPLICANT: MUTTY, Lynn E. ; APPLICANT: INVENTION: TUMOR-ASSOC ; NUMBER OF SEQUENCES: 6 ; CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaceuti	Matches 180; CONSERVATIVE QY 1 GAAAGCTCCCTTTCTCAA	-019-1 older 1, Application US/0906 older 1, Application US/0906 older 1, Application US/0906 nocentarion: ANT: Kato, Seishi ANT: Kato, Seishi ANT: Sekine, Shingo ANT: Sekine, Shingo ANT: Kamata, Kouju per INVENTION: HUMAN PEC- EFERENCE: 6700PCT-US FAPPLICATION NUMBER: US FAPPLICATION NUMBER: US FILING DATE: 1998-04-1 OF SEQ ID NOS: 3 OF SEQ ID NOS: 3 RE: PatentIN Ver. 2.0 NO 1 NO 1 SR: PatentIN Ver. 2.0 NO 1 SR: Homo sapiens Old-1 itch 100.0%;	28 28.2 15.7 466 4 29 28.2 15.7 771 2 30 28.2 15.7 771 4 31 28.2 15.7 2495 4 32 28.2 15.7 2495 4 33 28.2 15.7 2525 2 34 28.2 15.7 2525 4 28.2 15.7 2525 4 27.4 15.2 2226 4 27.4 15.2 2226 4 27.4 15.1 2818 2 27.4 15.2 15.1 2818 2 27.4 15.2 15.1 2818 2 27.4 15.2 2531 4 26.6 14.8 2581 4 26.6 14.8 2581 4 26.6 14.8 2581 4
44670 ASSOCIATED KAZAL INHIBITOR Ceuticals, Inc.	O; MISMATCHES GAATGCCCATCTGTGAA	LIGNMENTS (6) (7) (6) (65) (180)	US-09-617-804-5 US-08-972-008-3 US-09-267-409-3 US-09-111-027-1 US-09-17-804-1 US-08-972-008-1 US-09-267-409-1 US-09-267-409-1 US-09-412-554A-3 US-09-412-554A-3 US-09-412-554A-3 US-09-21-0178-506 US-09-21-0178-506 US-09-221-0178-506 US-09-252-991A-9494 US-09-252-991A-9541 US-09-252-991A-9541 US-09-252-991A-9541 US-09-252-991A-9541 US-09-252-991A-9541 US-09-252-991A-9541 US-09-252-991A-9541 US-09-252-991A-9541 US-09-252-991A-9541
- 12 xc	els 0; Gaps 0; AGAGTCTCCAACCTGT 60	ENCODING THIS PROTEIN	Sequence 5, Appli Sequence 3, Appli Sequence 1, Appli Sequence 206, Appli Sequence 18, Appli Sequence 9494, Appli

3174 Porter Drive

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GENERAL INFORMATION:
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IMMEDIATE SOURCE:
LIBRARY: SINTTUT01
CLONE: 1539065
             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatit
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                         APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: TUMOR
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CITY: Palo Alto
STATE: CA
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                                                                                   STATE: C
                                                                                                             STREET: 3174 Por CITY: Palo Alto
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OPERATING SYSTEM: DOS
                                                                                                                                                ADDRESSEE:
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FastSEQ Version 2.0
                      IBM Compatible
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100.0%; Pred. No. 4.5e-56;
tive 0; Mismatches 0;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-065-019-2
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Applic
Patent No. 6280968
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CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN PEC-60-LIKE PROTEIN AND DNA ENCODING THIS PROTEIN FILE REFERENCE: 6700PCT-US
                                                                                                                                                                                                                                                                                                                             APPLICANT: Kato, Seishi
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Sekine, Shingo
APPLICANT: Kamata, Kouju
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LIBRARY: SINTT
CLONE: 1539065
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ATTORNEY/AGENT INFORMATION:
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Pred. No. 4.5e-56;
Pred. No. 4.5e-56;
                                                                                                             pred. No. 4.5e-56;
mismatches 0;
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; ORGANELLE:
; IMMEDIATE SOURCE:
US-08-880-829-21
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US-08-880-829-21
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 687-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDDERFECT 5.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,668
FILING DATE: 06/02/95
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MEDIUM TYPE: 3-1/2" DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06/07/94 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Joseph T. Eisele
ADDRESSEE: Kane, Dalsimer, Sullivan,
ADDRESSEE: Levy, Eisele and Richard
STREET: 711 Third Avenue
CITY: New York
COUNTEY. New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/880,829 FILING DATE: 23-JUN-1997 CLASSIFICATION: 435
                                                                      TISSUE TYPE:
CELL TYPE:
                                                                                                                          INDIVIDUAL ISOLATE: DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single strand
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: EISELE, JOSEPH T. REGISTRATION NUMBER: 25
                                                       CELL LINE:
                                                                                                          HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                         LENGTH: 458 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RY: U.S.A.
10017-4059
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5925559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VENTION: A Collection of Phagemids, A VENTION: Collection of Escherichia Coli VENTION: Cells Carrying The Phagemids, A VENTION: Collection of Phagemid Particles VENTION: Produced From Said Collection
                                                                                                                                                                                                                                                                                                                                                                                                              (212) 682-3485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collins, John
                                                                                                                                                                                                                                                                                        linear
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21
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US-08-235-515A-26
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Best Local Sim
Matches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 302 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                             LOCATION: 1..302
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: /UJ = TELEPH
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OPERATING SYSTEM:
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STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/235,515A FILING DATE: 29-APR-1994
                                                                                           LOCATION:
                                                                                                                           NAME/KEY:
                                                                                                                                                                                         OTHER
                                                                                                                                                                                                                                                                                                            NAME/KEY:
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5840518
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57.7%;
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                                                                                                                                                                            Figure
                                                                                                                                                                                                                /label= polynucleotide
/note= "j-xl-y-z(psti),
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Pred. No. 6.2e-05;
0; Mismatches 52
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; CLONE: g190687
US-09-016-434-1250
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US-08-235-515A-26
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Best Local Similarity
    Matches
                             Query Match
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                                                                                                                                                                                    TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                             REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: HEREW
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OPERATING SYSTEM: PC-DOS/MS-DOS
                 Local
                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                        nucleic acid
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                                                                                                                                                        432 base pairs
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Jeffrey J. Seilhamer
VENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
  Conservative
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Score 36.6; DB 4;
Pred. No. 0.00089;
0; Mismatches 54;
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                          Length 432;
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LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 628424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 3.0
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US-60-487-610-243
PCT-US02-36071A-139
US-60-487-610-1955
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US-60-487-610-1956
US-10-469-285-639
US-60-485-450-3602
PCT-US02-14753A-362
PCT-US02-14753A-362
PCT-US02-14753A-362
PCT-US02-14753A-362
US-60-487-610-1923
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)			Query M Best Lo Matches	RESULT 1. US-60-487-610-19749/c Sequence 19749, Appli GENERAL INFORMATION: APPLICANT: CRAGILL, APPLICANT: HUANG, H TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: FILE REFERENCE: CLOO CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE: NUMBER OF SEQ ID NOS SOCTWARE: FastSEQ fo SEQ ID NO 19749 LENGTH: 28753 TYPE: DNA ORGANISM: Homo Sapi		443	410	38	3 6 5 4	 	310	28
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RESULT 2
US-60-485-450-12159/c
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CURRENT APPLICATION NUMBER: US/60/485,450

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                                                  ; OTHER INFORMATION: Genbank Accession No. M64780 US-60-493-007-3005
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NUMBER OF SEQ ID NOS: 47859
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12159
LENGTH: 28753
               Query Match
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Best Local Similarity
                                                                                                                                                                    SEQ ID NO 300
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/363,534
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/371,135
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/371,134
PRIOR FILING DATE: 2002-04-10
                                                                                                                                                                                                    Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 3518
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/394,253 PRIOR FILING DATE: 2002-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/60/493,007
CURRENT FILING DATE: 2003-08-07
                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Primary rat hepatocyte toxicity modeling FILE REFERENCE: 44921-5113-01-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mendrick, Donna
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                                                                                                                             TYPE: DNA
                                                                                          ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                              FILING DATE: 2002-04-19
APPLICATION NUMBER: US 60/374,139
FILING DATE: 2002-04-22
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/371,413 FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/371,150 FILING DATE: 2002-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/370,248 FILING DATE: 2002-04-08
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/373,601
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Elashoff, Michael
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91.9%;
17.0%;
73.6%;
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Pred. No. 2.5e-31;
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Score 30.6; D
Pred. No. 1.6;
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               DB 7;
               Length 7286;
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APPLICANT: CARGILL, Michele
TITLE OF INVENTION: PCYMORPHISMS IN NUCLEIC
TITLE OF INVENTION: ENCODING HUMAN G-PROTEI
TITLE OF INVENTION: OF DETECTION AND USES T
FILE REFERENCE: CL001484
CURRENT APPLICATION NUMBER: US/60/500,315
CURRENT FILLING DATE: 2003-09-05
NUMBER OF SEO ID NOS: 69978
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11231
LENGTH: 203938
TYPE: DNA
ORGANISM: Homo sapiens
US-60-500-315-11231
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; LENGTH: 15859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-500-315-11222
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US-60-500-315-11231
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2003-09-05
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TITLE OF INVENTION: ENC.
TITLE OF INVENTION: OF I
FILE REFERENCE: CL001484
                                                                                                                                                                                                                           Local Similarity
176415
                                                                   176355
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                                                                                 89 CTGATGGGCTCACATATACGAATGAATGCCAGCTCTGCTTGGCCCGGGATAAAAACCAAAC 148
                                                                                                                                                          29 TCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGTCCAACCTGGTCTGCGGCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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                                                               CAGCTTTCTGTACAGTGTTATTTGCAAGCCCACTAAGCTGGACAGGGAAAAGAACCTGAC
                                                                                                                                    TCTGGCTACCCATGGCAGCCCAGGAAAGAGAGTCCTGGATGCACAGGAGCTTCTCTGGGT 176354
                              AGGACATCCAGATCATGAA
                                                                                                                                                                                                         Conservative
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POLYMORPHISMS IN NUCLEIC ACID MOLECULES
ENCODING HUMAN G-PROTEIN COUPLED RECEPTOR PROTEINS, METHODS
OF DETECTION AND USES THEREOF
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ENCODING HUMAN G-PROTEIN COUPLED RECEPTOR PROTEINS, METHODS
OF DETECTION AND USES THEREOF
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51.1%;
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Pred. No. 6.8;
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Pred. No. 2.9;
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RESULT 6 US-60-500-315-11538/c

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Post-processing: Minimum Match 0%
Maximum Match 100%
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(without alignments)
9394.424 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. O C 00 367 248.8 248.8 211.2 1800 11145.88 811.25.88 81 Score Query Match 99.9 180 163396 176584 183099 188540 192093 230493 242175 Length 5008 501 182 182 182 182 182 186 368 368 368 368 368 368 368 368 368 432 341 432 2008 432 2008 ASVPSKAN8 ASVPSKAN8 MMPIMP12 E01574 EC025790 AR270687 HSPSTI 108731 E03479 AR028526 AR075817 BD007521 AF048700 \$46866 \$SPEC60 O MMMPGC60 AR16137 E13090 AL161445 AC027812 AC027812 AC0211108 AC121205 AC121205 AC1837521 AC121205 AC1837521 BD027884 HUMPSTI AX014216 AX655393 SYNPSTIAA A24907 AX332609 AX333248 AX411203 BD160949 A11352 A24905 AX014851 AR166138 SYNPSTIB AR166137 Sequence E13090 Human an CD AL161445 Human DNA AC027812 Homo sapi AC0211108 Homo sapi AC011108 Homo sapi AC0211205 Rattus no AL837521 Mouse DNA AC02663 Rattus no BD027885 Sequence BD027885 Sequence ED027885 Sequence A11350 Artificial A11352 Artificial A11352 Artificial A24905 PSTI master M21832 Synthetic h A24907 PSTI master AX333248 Sequence AX411203 Sequence AX411203 Sequence AX411203 Sequence BD160949 Preventiv Y00705 Homo sapien 108731 Sequence 19 E03479 CDNA encodi X84307 Artificial X06312 Mouse mRNA E01574 CDNA sequen AX014216 Sequence AX655393 Sequence AF094609 Rattus no E01725 Synthetic D E02456 DNA encodin M31103 Synthetic h AX014851 Sequence AR028526 Sequence AR075817 Sequence BD007521 Tumor-ass AF048700 Homo sapi \$46866 PEC-60-gast X67109 S.scrofa PE Y11505 M.musculus BC025790 Homo sap1 AR270687 Sequence AR166138 Sequence E13091 Human cDNA M11949 Human pancr Description

ALIGNMENTS

				fiers	Location/Qualifiers	Locati		FEATURES
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	same	ng the s	encodir	Human PEC-60-like protein and DNA encoding the same	ke prote	:-60-13	Human PEC	TITLE
		ita,K.	nd Kama	Kato, S., Yamaguchi, T., Sekine, S. and Kamata, K.	chi,T.,	Yamagu	Kato, S.,	AUTHORS
					398)	1 to	1 (bases 1 to 398)	REFERENCE
						ied.	Unclassified.	
							Unknown.	ORGANISM
							Unknown.	SOURCE
							•	KEYWORDS
					16241313	1 GI	AR166138.1 GI:16241313	VERSION
							AR166138	ACCESSION
				Sequence 2 from patent US 6280968.	n patent	2 from	Sequence	DEFINITION
PAT 17-OCT-2001		linear	DNA	398 bp			AR166138	LOCUS
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                                  Kato, M., Yamaguchi, T., Sekine, S. and Kamata, M.

HUMAN PEC-60LIKE PROTEIN AND DNA CAPABLE OF COL

Patent: JP 1997124698-A 2 13-MAY-1997;

SAGAMI CHEM RES CENTER
OS Homo sapiens (human)
PN JP 1997124698-A/2

PD 13-MAY-1997
PF 27-CCT-1995 JP 1995280272
PI KATO MASASHI, YAMAGUCHI TOMOKO, SEKINE SHI
MITSUHISA
PC C07K14/575,C07H21/04,C12N15/09//A61K38/22,
PC C12P21/02,C12R1:19);
PC (C12P21/02,C12R1:19);
PC (C12P21/02,C12R1:19);
PC (C12P21/02,C12R1:19);
PC (C12P21/02,C12R1:19);
PC Strandedness: Double;
PH Key

FH Key

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/organism='Homo sapiens'
FT Source

/tissue_type='stomach canc
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Kato,M., Yamaguchi,T., Sekine,S.
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Sequence
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                                                                                                                                    Human nucleic acid sequences from ovarian patent: WO 9953040-A 41 21-OCT-1999; SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DA BERND (DE); ROSENTHAL ANDRE (DE); METAGEN (DE); FILARSKY CHRISTIAN (DE)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
110 c 105 g 7
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                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                     GI:10041118
                                                                                                                  .402
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              Score 398;
Pred. No.
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Pred. No. 2.8e-99;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              402 bp
WO9953040.
  Mismatches
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              398; DB 6;
No. 2.8e-99;
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METAGEN GES FUER
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GENOMFORSCHUN
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Indels

0;

Gaps

0;

360 370 300

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RESULT 4
AR028526
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DEFINITION
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TITLE
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 388; Conserv
                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                source
                                 181
             251
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Sequence
AR028526
                                                                                                                                                                                                                                                                                                 1 (bases 1 to 388)
Bandman,O., Goll,S.K. and Murry,L.E.
Tumor-associated kazal inhibitor-like polypeptides and encoding
                                                                                                                                                                                                                                                                                  polynucleotides
Patent: US 5858
                                                                                                                                                                                                                                                                                                                                            Unknown
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                                                                                                                                                                                                                                                                                                                                    Unclassified
                                                                                                           GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGT
CCCGGATAAAAACCAAACAGGACATCCAGATCATGAAAGATGGCAAATGCTGATCCCACA
                             CTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGT
                                                                                                                                                             GCCAGCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGGGTAATCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGGATATGACATGAAATAAAAGATCCAGCCCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAATCGCCCTGGCCTTGGCCGCCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCA
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                                                                      CTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGT
                                                                                                                                                   GCCAGCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGGGTAATCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTGCTTGGCCCGGATAAAAACCAAACAGGACATCCAGATCATGAAAGATGGCAAATGC
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                                                                                                                                                                                          97.5%;
ilarity 100.0%;
Conservative
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Location/Qualifiers
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                                                                                                                                                                                                                                         /organism="unknown"
105 c 102 g
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                                                                                                                                                                                                                                                                                                                                                                                             patent
                                                                                                                                                                                         Score 388; DE; Pred. No. 1.6
0; Mismatches
                                                                                                                                                                                          0;
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5858710.
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1.6e-96;
hes 0;
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                                                                                                                                                                                                            Length 388;
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BD007521
LOCUS
DEFINITION
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 VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
FEATURES
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AR075817
LOCUS
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Best Local S
Matches 388
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        BD007521
Tumor-associated KAZAL t.
BD007521
BD007521.1 GI:18635894
JP 2001503629-A/1.
unidentified
                                                                                                             361
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Sequence 2 :
AR075817
AR075817.1
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1 (bases 1 to 388)
Bandman,O., Goli,S.K. and Murry,L.E
Tumor-associated Kazal inhibitor
Patent: US 5958699-A 2 28 SEP-1999;
Location/Qualifiers
  unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                CTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGT
                                                                                                                                                                                                                                                                                                                                                   GGAGCACCTCAAGCCATGAAGTGTCAGCTGGAGAACAGTGGTGGGCCATGGAGAGATATG
                                                                                                                                                             GGAGCACCTCAAGCCATGAAGTGTCAGCTGGAGAACAGTGGTGGGCATGGAGAGATATG
                                                                                                                                                                                                   CCCGGATAAAAACCCAAACAGGACATCCAGATCATGAAAGATGGCAAATGCTGATCCCACA
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patent US 5958699
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Pred. No. 1.6e-96;
                                                388
type :
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                                                  bp DN.
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Gaps

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130

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180 190 120

300 310 240 250

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RESULT 7
AF048700
LOCUS
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ACCESSION
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AUTHORS
TITLE
JOURNAL
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                                       SOURCE
                           ORGANISM
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PN J-PAO
PD 21-MA
PF 05-NO
PF 05-NO
PR 06-NO
PC C12N1
PC C12N1
PC C12N1
PC C12N1
PC A61K3
CC A61K3
CC Key
FT Sourc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 388)
Bandman,O., Goli,S.K. and Murry,L.E.
Tumor-associated KAZAL type inhibitor
Patent: JP 2001503629-A 1 21-MAR-2001;
INCYTE PHARMACEUTICALS INC
                          Homo sapiens
                                                                         Homo sapiens
AF048700
             Eukaryota;
                                      Homo sapiens (human)
                                                              AF048700.1
                                                                                                AF048700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                           GGAGCACCTCAAGCCATGAAGTGTCAGCTGGAGAACAGTGGTGGGCATGGAGAGAATATG
                                                                                                                                                                                                                                                          CCCGGATAAAAACCAAACAGGACATCCAGATCATGAAAGATGGCAAATGCTGATCCCACA 310
                                                                                                                                                                                                                                                                                                         CTTTCTCAAGAATGCCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGT
                                                                                                                                                                                                                                                                                                                                                                      CTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGT 190
                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCCTTGGCTGCCCTTGTTGTGGGACAGGGAAGTGCCAGTGGCAGCAGGAAAGCTCC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCAGCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGGGTAATCGCCC
                                                                                                                                                             ACATGAAATAAAAGATCCAGCCCAACTG
                                                                                                                                                                                    ACATGAAATAAAAGATCCAGCCCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                         TGGCCTTGGCTGCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCAGGAAAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCAGCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGGGTAATCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001
05-NOV-1997 JP 1998521770
05-NOV-1996 US 08/744670
06-NOV-1996 US 08/744670
01-GA BANDMAN, SURYA K GOLI, LYNN E MURRY
C12N15/09, A61K38/55, A61K39/395, A61P1/00, A61P35/00, C07K14/81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/68,G01N33/574, PC
15/00,C12N5/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism='Unidentified'.
Location/Qualifiers
1...388
 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
105 c 102 g 7
                                                              GI:2935439
                                                                                   386 l
gastrointestinal
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 Chordata;
Primates;
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1. .388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 388; I
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                   bp mRNA linear
l peptide (PEC-60) mRNA,
Craniata; Ve Catarrhini;
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           Vertebrata;
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 Hominidae;
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Sus scrofa
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Mammalia; Eutheria; C
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Submitted (17-FEB-1998) Shanghai Institute
Sue-Yang Road, Shanghai 200031, China
Location/Qualifiers
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PEC-60=gastrointestinal
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llarity 100.0%;
Conservative
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/protein_id="AAC05124.1"
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98 g 72 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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12. .272
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           Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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Pred. No. 1.1e-90;
0; Mismatches 0;
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| peptide
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           Euteleostomi;
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Molecular cloning of PEC-60 and expression of its mRNA and pe in the gastrointestinal tract and immune system J. Biol. Chem. 267 (28), 19829-19832 (1992)
                                     pec-60 gene.
Sus scrofa (pig)
Sus scrofa
                                                                                       SSPEC60
S.scrofa PEC-60
X67109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created thi
entry [NCBI 91b5sq 115614] from the original journal article.
This sequence comes from Fig. 1.
Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 364)
                                                                           x67109.1
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/product="PEC-60"
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/translation="MAVRLWYVALALAALFIVDREVPVSAEKQVFSRMPICEHMTESP
DCSRIYDPYCGTDGYVYESECKLCLARIENKQDIQIVKDGEC"
108 g 72 t
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Fig. 1; Author includes translated amino acids
putative initiation codon"
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23. .283
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/db_xref="taxon:9823"
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Pred. No. 6.2e-58;
0; Mismatches 62
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AUTHORS
TITLE
                                                                      mpgc60 gene.
Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Krause,R., Hemberger,M., Messerschmid,M., Kothary,R. an Molecular cDNA cloning and expression of murine Mpgc60, predominantly expressed in the intestinal tract
                                                                                                                                                                                             M.musculus mRNA for Mpgc60
Y11505
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Submitted (22-JUN-1992) M. Metsis, Dept. of Medical Chemistry, Lab
of Molecular Neurobiology, Karolinska Institute, Box 604 00, 10401
                                                                                                                                                                             Y11505.1 GI:2344863
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                                                                                                                                                                                                                                                                                                                                                CATGAAGTGTC-AGCTGGAGAACAGTGGTGGGGGATGGAGAGGATATGACATGAAATAAAA 383
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DCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGEC"
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93 c 108 g 72
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Pred. No. 6.2e-58;
0; Mismatches 62
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1 (bases 1 to 180)
Kato,S., Yamaguchi,T., Sek
Human PEC-60-like protein
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Sequence 1 from patent US
AR166137
AR166137.1 GI:16241312
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Direct Submission
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Ihnestr. 73, 14195 Berlin,
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/db_xref="SPTREMBL:035679"
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NCPQPPNICECTDGLITYENECHLICITENKTMKDIQIMKDGQC"
a 129 c 136 g 95 t
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/db_xref="taxon:10090"
/tissue_type="intestine"
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/mol_type="mRNA"
/strain="NMRI"
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HUMAN PEC-60LIKE PROTEIN AND DNA CAPABLE OF
Patent: JP 1997124698-A 1 13-MAY-1997;
SAGAMI CHEM RES CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 180)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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JP 1997124698-A/1.
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13-MAY-1997
27-OCT-1995 JP 1995280272
77-MTO MASASHI, YAMAGUCHI TOMOKO, SEKINE SHINGO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.2%; Score 180; DB 6; Llarity 100.0%; Pred. No. 7.5e-39; Conservative 0; Mismatches 0;
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C12P21/02,C12R1:19);
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                                              Conservative
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                                                                                                                                                                                                                                                    topology: Linear;
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Location/Qualifiers
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                                                                                                   /organism="Homo sapiens"
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/db_xref="taxon:9606"
1 49 c 40 q
                                                                                                                                                         /product='PEC-60-like protein'
Location/Qualifiers
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49 c 40 g
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                                              Score 180; DB 6;
Pred. No. 7.5e-39;
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                  AAT64673
AAZ77490
AAC98176
AAH34805
AAW38073
ABV97573
ABQ60075
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ovarian tumo
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colon cancer
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T64673;	1 3 T64673 standard; cDNA to mRNA; 398 BP.	ALIGNMENTS	44444444444444444444444444444444444444	1.4 80.8 323 24 ABV89 4.8 64.0 283 24 ABQ60
			Human colon cancer Human spired tran Human secreted pro Sequence encoding Synthetic DNA enco Human pancreatic s Human pancrer relate Lung cancer relate Lung cancer relate Synthetic DNA enco Human pancreatic s Human colon cancer Human colon cancer Human signalling p Human prostate exp Human prostate exp	

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121..300
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Human; PEC-60-type protein; digestive disorder; immune disorder; nervous disorder; gastrointestinal tract hormone; gastric tissue; antigen; antibody; ds.

Human PEC-60-type protein encoding cDNA.

22-DEC-1997 (first entry)

27-OCT-1995;

95JP-0280272.

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RRESULT 2
AAZ7740
ID AAZ77
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AC. AAZ7
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EXP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes a human PEC-60-type protein. The protein is a gastrointestinal tract hormone secreted by the gastric tissues. It is useful for treatment or diagnosis of digestive, immune or nervous disorders, or as an antigen to raise antibodies against them. Large amounts of the protein may be produced by using the corresponding cDNA.
                                              Homo
                                                                                                                                                      AAZ77490
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 21-OCT-1999
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                                                                    gene
                                                                                Expressed
                                                                                                                               10-APR-2000
                                                                                                                                                                           AAZ77490 standard; cDNA; 402 BP
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DB; AAW15067.
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                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCCAACCTGT
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                                                                                sequence tag; EST; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 A; 110 C; 105 G; 76 T; 0 other;
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disorders
                                                                                                                              entry)
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                                                                                                     cDNA library derived EST
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Pred. No. 1.2
0; Mismatches
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1.2e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel nucleic acid (cDNA) sequences (A) which CC have anticancer activity and are highly expressed in ovarian tumor ctissue (and some also in testis and breast cancer tissue). The products CC tissue (and some also in testis and breast cancer tissue). The products CC of the invention can be used for gene therapy. (A) are used (i) for crecombinant expression of polypeptides (B) and (ii) to isolate complete CC quess. (B) are used (i) to identify agents suitable for treatment of CC (including expression from gene therapy vectors) and (iii) for generation CC (including expression from gene therapy vectors) and (iii) for generation CC (including expression from dentified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of CC expression patterns. This allows a significantly longer fragment of the CC expression patterns. This allows a significantly longer fragment different CC with the fact that ESTs from different libraries may represent different CC parts of the same unknown gene, distorting the estimated frequency of CC occurrence in a particular tissue. AAZ77450-Z77572 represent the human CC ovarian tumor cDNA library derived EST fragments described in the method of the invention and except the protein fragments represented in
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid sequences expressed in ovarian, and some other, c
tissues, and derived polypeptides, for treatment of ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenthal A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                        GTAATCGCCCTGGCCTTGCCCTCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCA
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Pred. No. 1.2e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 610; 2104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
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reproductive disorder; gastrointestinal disorder; renal disorder;
infectious disease; cardiovascular disorder; ss.
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DB; AAB53419.
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GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCCAACCTGT
                                                               GTAATCGCCCTGGCCTTGGCTGCCCTCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCA
                                                                                                         GCAGGCCCCAGCCTCAGGCTACACTATCCCCAGGATCAGCATGGCCGTCCGCCAGTGG
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                                                                                                                                                                        Conservative
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tem disorder; muscular disorder;
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                                                                                                                                                                                     Score 395;
Pred. No.
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                                                                                                                                                                                                 Length 433;
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RESULT 4
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                                                                                                                                                                                 therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat discorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer-associated nucleic acid molecules (N) and proteins (P), who the proteins are collectively known as colon cancer antigens. The cancer antigens have cytostatic activity and can be used in gene
                                                                                                                                             and AAB77789 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 4277 human useful for preventing, diagnosing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                       411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                inhibitor"
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The present sequence encodes human tumour-associated Kazal inhibitor (TAKI). TAKI is expressed in response to inflammatory cytokines and functions in the inhibition of serine proteases or glycoprotein hormones present in diseased tissues. The TAKI can be used to inhibit the tissue destruction associated with the production of excess proteases such as trypsin, chymotrypsin, elastase, or pepsin. Products from the present invention can be used in the treatment of e.g. proliferative cell division in inflamed intestinal tissues, ulcerative colitis, Crohn's disease or cancer. The products can also be used for detection and
                                                                                                                                                                                                                                                                                                                                               New isolated tumour-associated Kazal inhibitor, TAKI - used develop products for the diagnosis and treatment of e.g. inflammation, ulcerative colitis, Crohn's disease or cancer
    Sequence 389
                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                   5; Fig 1;
    BP;
                                                                                                                                                                                                                                                                                                 62pp;
105 A; 105 C; 102 G; 76 T; 1 other;
                                                                                                                                                                                                                                                                                                      English.
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Query Match Best Local Matches

388;

Conservative

0;

Similarity

100.0%;

97.5%; Score 388; DB 19;

Length

Pred. No. 1.7e-112; Mismatches

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Indels

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Gaps

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ABV97573 standard;
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cDNA; 394 ВP

ABV97573;

14-JAN-2003 (first entry)

Human pancreatic cancer expressed CDNA SEQ ID NO 2981

Human; pancreas;
cytostatic; tumou tumour; cancer; gene therapy; ur; gene; ss. vaccine; immunostimulant;

sapiens

WO200260317-A2

08-AUG-2002.

30-JAN-2002; 2002WO-US02781

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                                                                                                                                                                                                                                                                    ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide (I) comprising: (a) CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); CC (b) complements of (a); (c) sequences consisting of at least 20 CC contiguous residues of (a); (d) sequences that hybridize to (a), under CC (a) contiguous residues of (a); (e) sequences that hybridize to (a), under CC (a) contiguous residues of (a); (e) sequences having at least 75% or 90% (c) dentity to (a); or (f) degenerate variants of (a). Polypeptides (c) (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to CC (aBP68596-ABP68637) encoded by (I) and oligonucleotide can be used to CC (aBP68596-ABP68637) encoded by (I) and oligonucleotide are useful in treating parties, antibodies, fusion proteins, T cell populations and CC entities pancreatic cencer and stimulating an immune response. The CC polynucleotides can be used as probes or primers for nucleic acid CC hybridisation, in the design and preparation of ribozyme molecules for CC inhibiting expression of the tumour polypeptides and proteins in the CC Note: The sequence data for this patent did not form part of the printed constitutions, but was obtained in electronic format directly from WIPO at free wine (attractive and not segmence).
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 350
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31-JAN-2001;
31-JAN-2001;
09-FEB-2001;
21-MAR-2001;
28-APR-2001;
16-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2001;
20-AUG-2001;
27-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 394 BP; 115 A; 102 C; 100 G; 73 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for diagnosing, pancreatic cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Benson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated polynucleotide and pancreatic tumor polypeptides, diagnosing, preventing and/or treating cancer, particulari: preatic cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-627435/67
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                                                                                                                       AGAGTCTCCAACCTGTTCCCAGATGTCCAACCTGGTCTGCGGCACTGATGGGCTCACATA
                                                                                                                                                                                                                                                            AGTGCCAGTGGCAGCAGGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGT
                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2981; 300pp + Sequence Listing; English
GAAAGATGGCAAATGCTGATCCCACAGGAGCACCTCAAGCCATGAAGTGTCAGCTGGAGA
                                                                                                                                                     TACGAATGAATGCCAGCTCTGCTTGGCCCGGATAAAAACCAAACAGGACATCCAGATCAT
                                                                                                                                                                                 AGAGTCTCCAACCTGTTCCCAGATGTCCAACCTGGTCTGCGGCACTGATGGGCTCACATA
                                                                                                                                                                                                                                            AGTGCCAGTGGCAGCAGGAAAGCTCCCTTTCTCAAGAATGCCCCATCTGTGAACACATGGT
                                                                                                                                                                                                                                                                                                        GGCCGTCCGCCAGTGGATAATCGCCCTGGCCTTGGCTGCCCTTCTTGTTGTGGACAGGGA
                            ACAGTGGTGGGCATGGAGGATATGACATGAAATAAAAGATCCAGCCCAA 395
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2001US-265682P.
2001US-267568P.
2001US-278651P.
2001US-287112P.
2001US-291631P.
2001US-313999P.
2001US-333626P.
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                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                 87.8%;
99.7%;
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Pred. No. 2.8e
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351
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ABQ60075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially CC expressed in cancer tissues, ABB7893 to ABB79004 represent proteins CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be CC used in antisense therapy. An antibody immunoreactive with a polypeptide CC encoded by (I) is useful for detecting cancer in a patient sample, and CC for detecting the presence or absence of a polynucleotide encoded by a CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived CC from (I) can be used for determining the presence of a nucleic acid which hybridises to (I); and for determining the phenotype of cells in a sample CC of cells from a patient. (I) is useful for determining the presence of CC colon cancer in a cell or tissue type, for determining the presence or CC state of other type of cancer, in antisense therapy, to generate CC macroarrays on a solid surface, to identify a chromosome on which the CC canthysis, mapping and diagnostic applications. (I) can be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibodies, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid that is differentially expressed itissues useful for determining the presence of colon cancer or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burgess C, Astle JH, Thiaglingam A, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2000; 2000US-237271P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                      181
                                                                           127
                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                        371;
                                                                                                                                                                                        67
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                                                                                                                                                                                                                  GTAATCGCCCTGGCCTTGGCTGCCCTCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  468
TCCCAGATGTCCAACCTGGTCTGCGGCACTGATGGGCTCACATATAC-GAATGAATGCCA
                                                                                                          GGAAAGCTCCCTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGT
                                                                                                                                                                                                                                                                                                                            GCAGGCCCCAGCCAGCCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGG
                                                                                                                                                                                      GTAATCGCCCTGGCCTTGACTGCCCTCCTTGTTGTGGATAGGGAAGTGCCAGTGGCAGCA
                                                                                                                                                                                                                                                                                                GGAGGCCCCAGCCAGCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGG
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                                                                           NGAAAGCTCCCTTTCTCAAGAATGCCCCATCTGTGAACACATGGTATAGTCTCCAACCTGT
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 120 A; 116 C; 119 G; 95 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US30732
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Pred.
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No. 8.7
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ID ABV868
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06-FEB-2001;
28-MAR-2001;
                                                                                                                       The invention relates to a human colon tumour expressed polynucleotide (I) encoding a polypeptide (II, ABB67991-ABB67996) comprising: (1) any o. 2600 fully defined nucleotide sequences (ABW8669-ABW89289); (11) complements of (1); (i11) at least 20 contiguous residues of (1); (iv) sequences that hybridize to (1), under moderately stringent conditions; (v) sequences having at least 75% or 90% identity to (1); or (vi) degenerate variants of (1). The compositions and methods of the present invention are useful for the diagnosis, prevention and/or treatment of cancer, particularly colon cancer. (I) can be used in gene therapy and (I) and (II) are useful in pharmaceutical compositions such as vaccines.

Note: The sequence data for this patent did not form part of the printed a specification, but was obtained in electronic format directly from WIPO at the print of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis,
                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated tumor colon
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d/or treatment of ca
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 Score 321.4; DB Pred. No. 1.8e-910; Mismatches
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GCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGGGTAATCGCCCTGGC

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20-NOV-2000;
06-FEB-2001;
28-MAR-2001;
The invention relates to a human colon tumour expressed polynucleotide (I) encoding a polypeptide (II, ABP67991-ABP67996) comprising: (i) any c 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii) complements of (i); (iii) at least 20 contiguous residues of (i); (iv) sequences that hybridize to (i), under moderately stringent conditions; (v) sequences having at least 75% or 90% identity to (i); or (vi) degenerate variants of (i). The compositions and methods of the present invention are useful for the diagnosis, prevention and/or treatment of cancer, particularly colon cancer. (I) can be used in gene therapy and (II) and (II) are useful in pharmaceutical compositions such as vaccines. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                 Claim
                                                                                                                                                                                 diagnosis,
                                                                                                                                                                                                                     WPI; 2002-608400/65
                                                                                                                                                                                                                                             Stolk JA,
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                                                                                                                                                                                 New isolated tumor colon polynucleotide and polypeptide, useful diagnosis, prevention and/or treatment of cancer, in particular
                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
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   330.8
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AW960685 EST372756
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BQ636767 he01b10.y
AA534438 nf80b04.s
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AUTHORS
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182.8
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                                             Unpublished Contact: John Quackenbush Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 3528 Fax: 301 838 0208
                                                                                                                Quackenbush, J.

Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray
                                                                                                                                                                                                                                           AW960685 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence. AW960685 AW960685.1 GI:8150369
                                                                                                                                                 1 (bases 1 to 553)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J.
                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Seq primer: Reverse.
    Location/Qualifiers
                        Email: johng@tigr.org
Plate: 149
                                                                                                                                                                                                                     Homo sapiens (human)
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AA296923 nf60b04 x
AA823442 vp40a09 r
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AA692439 vt59c08 r
CCB223030 LJEJ1864
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AA689871 vt62e06 r
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AA982819 vt57b03 r
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AA71385 AV070840
AA733374 vt74c08 r
AV066842 AV066346
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                                                                   Email: yongsung@mail.kribb.re.kr
Plate: 51 row: E column: 10
                                                                                                                                                        Genome Research Center
                                                                                                                                                                        Contact: Kim YS
                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                 Kim, N.S., Hahn, Y., Oh, Oh, K.J., Cheong, J.E., Kim, Y.S.
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1: +82-42-860-4470
x: +82-42-860-4409
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m, N.S., Hahn, Y., Oh, J.H.,
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, W/
/note="Vector: pBluescriptSKm"
a 153 c 137 g 107 t
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/organism="Homo sapiens"
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                                          Location/Qualifiers
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Pred. No. 1.1e-101;
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                                                                                                                           of Bioscience & Biotechnology
, Daejeon 305-333, South Korea
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Expressed sequence tag analysis of human retina for Project: Retbindin, an abundant, novel retinal cDNA splicing of other retina-preferred gene transcripts Mol. Vis. 8 (4), (2002) In press Contact: Wistow G
                                                                                                       1 (bases 1 to 334) Wistow, G., Bernstein, S.L., Wyatt, M.K.,
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="$14K402-51-E10"
/cell_line="K402"
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Pred. No. 1.3e-89;
0; Mismatches 0;
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sequence.
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similar to
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Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Plate: 01 row: b column:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="he01b10"
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/dev_stage="Adult"
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                                                                    321 bp mRNA linear EST 21-AI NCI_CGAP_CO3 HOMO Sapiens cDNA clone IMAGE:926191 SW:PE60_PIG P37109 PEPTIDE PEC-60 PRECURSOR. ;, ml
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Pred. No. 8.7e-83;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
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                                                                                          GCTGCCCTCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCAGGAAAGCTCCCTTTCTCA 138
                                                                                                                                                                                                                                          GTCTGCGGCACTGATGGGCTCACATATACGAATG-AATGCCAGCTCTGCTTGGCCCGGAT 257
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/Clone_libe="NCI_CGAP_CO3"
/Clone_libe="NCI_CGAP_CO3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Rot I; Site_2: Eco RI; lst strand cDNR
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNR was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library went through one round of
normalization. "
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/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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99.4%;
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601070792F1 NIH_MGC_12
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Plate: LLAM8445 row: h column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, 1
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1115)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
300 c 247 g 88 t
                                           Athersys RAGE Library I
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/clone="IMAGE:3456839"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
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/mol_type="mRNA"
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1 (bases 1 to 537)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachadran, R., Whittington, J. Leventhal, C., Thornton, M., Ramachadran, R., Waistington, J., Leventhal, C., Thornton, M., Boozer, S., Mays, R., Smith, E., Veloso, N., Kilka, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Creation of genome-wide protein expression libraries using random activation of gene expression nat. Biotechnol. 19 (5), 440-445 (2001)
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               Homo
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EST112478 Retina
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Fax: 216 361 9596
Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact:
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/note="See 'Creation of Genome wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No.
                                                                                 232 bp mRNA linear EST sapiens cDNA 5' end similar to PEC-60, mRNA sequence.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-744-670-2
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US-09-065-019-1
US-08-880-829-21
US-09-016-434-1250
US-09-221-298-56
US-09-221-298-56
US-09-221-298-63
US-09-016-434-361
US-09-08-899-709-2
US-08-49-2038-2
US-08-49-2038-2
US-08-49-2038-1
US-09-085-407-2
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US-08-452-427-1
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Patent NO. 6280968
GENERAL INFORMATION:
APPLICANT: Kato, Seishi
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Sekine, Shingo
APPLICANT: Kamata, Kouju
TITLE OF INVENTION: HUMAN PEC-60-LIKE PROTEIN ANI
FILE REFERENCE: 6700PCT-US
CUERRENT APPLICATION NUMBER: US/09/065,019
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LENGTH: 398
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Best Local
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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  AGAGGATATGACATGAAATAAAAGATCCAGCCCAACTG
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US-09-512-283C-357
US-09-520-312D-894
US-08-586-676E-4
US-08-586-676E-5
US-08-586-676E-6
US-08-32-463-1
US-08-32-463-1
US-08-32-463-3
US-09-398-339-3
US-09-398-339-3
US-09-318-448-9
US-09-352-616A-362
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US-09-352-616A-362
US-09-352-616A-362
US-09-252-991A-2370
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Pred. No. 4.5e-121;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: SINTTI
CLONE: 1539065
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: TUMOR-ASSOCIATED KAZAL INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/7. FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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   241
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Pred. No. 8.6e-118;
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                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/1/
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
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LIBRARY: SINTTUT01
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LENGTH: 388 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskett
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APPLICANT: MUXTY, LYND E.
TITLE OF INVENTION: TUMOR-ASSOCIATED KAZAL INHIBITOR
NUMBER OF SEQUENCES: 6
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LIBRARY: Sin.
NE: 1539065
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                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                        TGGCCTTGGCCGCCCTTGTTGTGGACAGGGAAGTGCCAGTGGCAGCAGGAAAGCTCC
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                             CTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGT
                                                                                                                                                    GCCAGCTCAGGCTACACTATCCCAGGATCAGCATGGCCGTCCGCCAGTGGGTAATCGCCC
                                                         CTTTCTCAAGAATGCCCATCTGTGAACACATGGTAGAGTCTCCAACCTGTTCCCAGATGT 190
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100.0%; Pred. No. 8.6e-118;
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SEQ ID NO 1
LENGTH: 180
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local
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Patent No. 6280968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kato, Seishi
APPLICANT: Yamaguchi, Tomoko
APPLICANT: Sekine, Shingo
APPLICANT: Sekine, Shingo
APPLICANT: Kamata, Kouju
TITLE OF INVENTION: HUMAN PEC-60-LIKE PROTEIN AND DNA ENCODING THIS PROTEIN
FILE REFERENCE: 6700PCT-US
CURRENT APPLICATION NUMBER: US/09/065,019
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                               Patent No. 5925559
GENERAL INFORMATION:
                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Joseph T. Eisele
                                                                                                   APPLICANT: Collins, John
APPLICANT: Roettgen, Peter
TITLE OF INVENTION: A Collection of Phagemids, A
TITLE OF INVENTION: Collection of Escherichia Coli
TITLE OF INVENTION: Cells Carrying The Phagemids, A
TITLE OF INVENTION: Collection of Phagemid Particles
TITLE OF INVENTION: Produced From Said Collection
TITLE OF INVENTION: And Phagemid Particles
                                                                                   NUMBER OF SEQUENCES:
                     ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
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5925559
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                  Kane, Dalsimer, Sullivan, Kurucz,
Levy, Eisele and Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.2%; Score 180; DB 3; 100.0%; Pred. No. 1.1e-49;
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; Sequence 1250, Applicat
patent No. 6500938
; GENERAL INFORMATION:
APPLICANT: Janice I
APPLICANT: Jeffrey
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/458
FILING DATE: 06/02/95
APPLICATION NUMBER: GERMAN
FILING DATE: 06/07/94
PILING DATE: 06/07/94
ATTORNEY/AGENT INFORMATION:
NAME: EISELE, JOSEPH T.
REGISTRATION NUMBER: 25,33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 682-3485
TELEX: (212) 426767
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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MEDIUM TYPE: 3-1/2° DISKETTE
COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDPERFECT 5.0
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CELL LINE:
                                                                                                                                                                                                                                                                                                                                            Local Similarity nes 75; Conserv
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Y: U.S.A.
                                                                                                                                                                                                                                                                              10.4%; nilarity 57.3%; Conservative
   Janice Au-Young
Jeffrey J. Seilhamer
                                                                   Application US/09016434
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                                                                                                                                                                                                                                                                                                                                            Score 41.4; DB 2;
Pred. No. 0.00056;
0; Mismatches 56;
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US-09-016-434-1250
                                                                                                                                                                        Sequence 26, Application US/08235515A Patent No. 5840518
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                             APPLICANT: No. 5840 TITLE OF INVENTION: TITLE OF INVENTION:
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                                                               TITLE OF INVENTION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                            APPLICANT:
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APPLICATION NUMBER:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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                     ADDRESSEE:
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P.O.
                                               Morishita, nauca Kanamori, Toshinori Kanamori, Toshinori No. 5840518uhara, Masahiro No. 5840518uhara, Masahiro CONTAINING THE DNA NVENTION: DNA FRAGMENT, TRANSFORMANT TRANSFORMED WITH TRANSFORMANT TRANSFORMED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 base pairs
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                Birch,
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                Stewart,
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                 Kolasch & Birch
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US-09-221-298-56/c
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OE INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 112
                                                                                                                         Sequence 56, Application US/09221298 Patent No. 6284241
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 29-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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NAME/KEY:
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CURRENT APPLICATION DATA:
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OTHER INFORMATION:
OTHER INFORMATION:
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STATE: Virginia
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72; Conserv
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27..293
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/note= "j-xl-y-z(psti),
Figure 5"
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Pred. No. 0.0018;
D; Mismatches 5
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